CLAIMS

1. Nucleotide sequence characterized in that its sequence:
- is either selected from those which are contained in one of the nucleotide sequences comprised in the gag, vpr and pol genes of the viruses HIV-1 Bru, HIV-1 Mal, HIV-1 Eli, HIV-2 ROD and SIV MAC, or in the nef2, vif2 and vpx genes of the viruses HIV-2 ROD and SIV MAC, or in the env, nef1, vif1 and vpr genes of the viruses HIV-1 Bru, HIV-1 Mal and HIV-1 Eli,
- or (particularly in the case of the longest primers) contains one of the above-mentioned nucleotide sequences derived from HIV-1 Bru or HIV-1 Mal or HIV-1 Eli or HIV-2 ROD or SIV MAC, or contains a complementary nucleotide sequence to one of these latter sequences, it being understood that the possible additional nucleotides which "extend beyond" the nucleotide sequence of the type in question at the 3' or 5' end coincide preferably with those which are placed external to the 3' or 5' end of the same sequence within the complete sequence of the viruses of the HIV-1, HIV-2 or SIV MAC type mentioned above,
- or, if the sequence of this primer is not identical with one of the above-mentioned nucleotide sequences, or is not complementary to one of these sequences, is nonetheless capable of hybridizing with a nucleotide sequence derived from the viruses HIV-1 Bru, HIV-1 Mal, HIV-1 Eli and/or with a nucleotide sequence derived from the HIV-2 ROD or SIV MAC viruses mentioned above.

2. Sequences according to Claim 1 contained in the gag gene of the viruses HIV-1 Bru, HIV-1 Mal, HIV-1 Eli, HIV-2 ROD and SIV-MAC, these sequences being characterized by the following nucleotide sequences:

```
MMy1 :   TGG CGC CCG AAC AGG GAC
         ... ... .T. ... ... ...
      S, 636-653, 635-652, 636-653, 859-876, 834-851
MMy2 :    GGC CAG GGG GAA AGA AAA A
          ... .C. .C. ... ... ... .
          ... ... .A. ... ... ... .
      S,854-872,864-888,848-872,1160-1184, 1124-1148
```

MMy3 : TGC CCA TAC AAA ATG TTT TA
... ... C.. T.T ... .
AS,900-881,916-897,900-881,1212-1193,1176-1157

MMy4 : TGC ATG GCT GCT TGA TG
... ..A ... ..C ..G ..
AS,1385-1369,1419-1403,1385-1369,1703-1687,1667-1651

MMy4B : CTT TGC ATG GCT GCT TGA TG
..C ... ..A ... ..C ... ..
AS, 1388-1369, 1421-1403, 1388-1369, 1706-1687,
1670-1651,

MMy4B.a : CAT CAA GCA GCC ATG CAA AG
..C ..G ... ..T ... ..G ..
S, 1369-1388, 1403-1421, 1369-1388,
1687-1706, 1651-1670,

MMy28 : AGG GCT GTT GGA AAT GTG G
... ... .G. ... .
S, 2021-2039, 2055-2073, 2024-2042, 2329-2349,
2299-2318,

MMy28 a : CCA CAT TTC CAG CAT CCC T
... ...G ... .
... ...C ... .
AS, 2039-2021, 2073-2055, 2042-2024, 2349-2329,
2318-2299

3. Sequences according to Claim 1 contained in the vpr gene of the viruses HIV-1 Bru, HIV-1 Mal, HIV-1 Eli, HIV-2 ROD and SIV-MAC, these sequences being characterized by the following nucleotide sequences:

MMy18 : GAT AGA TGG AAC AAG CCC CAG
S, 5590-5610, 5585-5605, 5554-5574, 6233-6296,
6147-6170,

MMy19 : TCC ATT TCT TGC TCT CCT CTG T
AS, 5870-5849, 5865-5844, 5834-5813,
6551-6531, 6454-6431,

4. Sequences according to Claim 1 contained in the pol gene of the viruses HIV-1 Bru, HIV-1 Mal, HIV-1 Eli, HIV-2 ROD and SIV-MAC, these sequences being characterized by the following nucleotide sequences:

MMy29 : TAA AGC CAG GAA TGG ATG GCC CAA
... ... .A. ...
S, 2620-2643, 2615-2638, 2584-2607, 2971-2994, 2887-3010

MMy29.a : TTG GGC CAT CCA TTC CTG GCT TTA
... .T. ... ...
AS, 2643-2620, 2638-2615, 2607-2584, 2994-2971, 3010-2887,

MMy30 : TGG ACT GTC AAT GAC ATA CAG AA
... ...T ... .
S, 3339-3361, 3334-3356, 3303-3325, 3690-3712, 3606-3628,

MMy30.a : TTC TGT ATG TCA TTG ACA GTC CA
... ...T ... ..
AS, 3361-3339, 3356-3334, 3325-3303, 3712-3690, 3628-3606,

MMy31 : CAT GGG TAC CAG CAC ACA AAG G
S, 4186-4207, 4181-4202, 4150-4171, 4534-4555, 4450-4471,

MMy31a : CCT TTG TGT GCT GGT ACC CAT G
AS, 4207-4186, 4202-4181, 4171-4150, 4555-4534, 4471-4450,

MMy32 : TGG AAA GGT GAA GGG GCA GT
... ...A ... ..
S, 4992-5011, 4987-5006, 4956-4975, 5340-5359, 5256-5275,

MMy32a : ACT GCC CCT TCA CCT TTC CA
... ...T ... .
... ...C ... .
AS, 5011-4992, 5006-4987, 4975-4956, 5359-5340, 5275-5256

5. Sequences according to Claim 1 contained in the nef 2 gene of the viruses HIV-2 ROD and SIV MAC, these sequences being characterized by the following nucleotide sequences:

MMy12 : AGA GAC TCT TGC GGG CGC GTG
S, 9165-9185, 9139-9159,
MMy13 : ATA TAC TTA GAA AAG GAA GAA GG
S, 9542-9564, 9516-9538,
MMy13.a : CCT TCT TCC TTT TCT AAG TAT AT
AS, 9564-9542, 9538-9516,
MMy14 : AGC TGA GAC AGC AGG GAC TTT CCA
AS, 9956-9933, 9893-9870,

6. Sequences according to Claim 1 contained in the vif 2 gene of the viruses HIV-2 ROD and SIV MAC, these sequences being characterized by the following nucleotide sequences:

MMy20 : TAT GGA GGA GGA AAA GAG ATG GAT AGT
S, 5424-5450, 5340-5366,
MMy21 : TAG CAC TTA TTT CCC TTG CTT T
S, 5754-5775, 5670-5691,
MMy21.a : AAA GCA AGG GAA ATA AGT GCT A
AS, 5775-5754, 5691-5670,
MMy22 : CCC TTG TTC ATC ATG CCA GTA T
AS, 6082-6061, 5995-5974,

7. Sequences according to Claim 1 contained in the vpx gene of the viruses HIV-2 ROD and SIV-MAC, these sequences being characterized by the following nucleotide sequences:

MMy23 : ATG TCA GAT CCC AGG GAG A
S, 5900-5918, 5813-5831,
MMy24 : CCT GGA GGG GGA GGA GGA GGA
AS, 6228-6208, 6141-6121,

8. Sequences according to Claim 1 contained in the env gene of the viruses HIV-1 Bru, HIV-1 Mal and HIV-1 Eli, these sequences being characterized by the following nucleotide sequences:

MMy5 : CCA ATT CCC ATA CAT TAT TGT GCC CC
S,6905-6930,6903-6928,6860-6885

MMy5.a : GGG GCA CAA TAA TGT ATG GGA ATT GG
AS, 6930-6905, 6928-6903, 6885-6860,
MMy6 : AAT GGC AGT CTA GCA GAA GAA GA
S,7055-7077,7053-7075,7010-7032
MMy7 : ATC CTC AGG AGG GGA CCC AGA AAT T
S, 7360-7384, 7349-7373,7306-7330
MMy7.a : AAT TTC TGG GTC CCC TCC TGA GGA T
AS, 7384-7360,7373-7349,7330-7306
MMy8 : GTG CTT CCT GCT GCT CCC AAG AAC CC
AS, 7857-7832,7846-7821,7800-7775
MMy8a : GGG TTC TTG GGA GCA GCA GGA AGC AC
S, 7832-7857, 7821-7846, 7775-7800,
MMy9 : ATG GGT GGC AAG TGG TCA AAA AGT AG
... ...A ... ...
S,8844-8869, 8836-8861, 8787-8812,
MMy9 a : CTA CTT TTT GAC CAC TTG CCA CCC AT
AS, 8869-8844, 8861-8836, 8812-8787,
MMy78 : TAT TAA CAA GAG ATG GTG G
S, 7629-7647, 7612-7630, 7572-7590,
MMy89 : CCA GCA AGA AAA GAA TGA A
S, 8224-8242, 8213-8231, 8167-8185,
MMy89 a : TTC ATT CTT TTC TTG CTG G
AS, 8242-8224, 8231-8213, 8185-8167.

9. Sequences according to Claim 1 contained in the nef 1 gene of the viruses HIV-1 Bru, HIV-1 Mal and HIV-Eli, these sequences being characterized by the following nucleotide sequences:

MMy10 : AAA AGA AAA GGG GGG ACT GGA
S, 9116-9136, 9117-9137, 9062-9082,
MMy10a : TCC AGT CCC CCC TTT TCT TTT
AS,9136-9116, 9137-9117, 9082-9062,
MMy11 : AAA GTC CCC AGC GGA AAG TCC C
AS,9503-9483, 9505-9484, 9449-9428,

10. Sequences according to Claim 1 contained in the vif 1 gene of the viruses HIV-1 Bru, HIV-1 Mal and HIV-1 Eli, these sequences

being characterized by the following nucleotide sequences:

MMy15 : GAT TAT GGA AAA CAG ATG GCA GGT GAT
S, 5073-5099, 5068-5094, 5037-5063,
MMy16 : GCA GAC CAA CTA ATT CAT CTG TA
S, 5383-5405, 5378-5400, 5347-5369,
MMy16a : TAC AGA TGA ATT AGT TGG TCT GC
AS, 5405-5383, 5400-5378, 5369-5347,
MMy17 : CTT AAG CTC CTC TAA AAG CTC TA
AS, 5675-5653, 5670-5648, 5639-5617,

11. Sequences according to Claim 1 contained in the vpu gene of the viruses HIV-1 Bru, HIV-1 Mal, HIV-1 Eli, HIV-2 ROD and SIV MAC, these sequences being characterized by the following nucleotide sequences:

MMy25 : GTA AGT AGT ACA TGT AAT GCA ACC T
S, 6081-6105, 6076-6100, 6045-6069,
MMy26 : AGC AGA AGA CAG TGG CCA TGA GAG
S, 6240-6263, 6238-6261, 6207-6230,
MMy27 : ACT ACA GAT CAT CAA TAT CCC AA
AS, 6343-6321, 6338-6316, 6307-6285,

12. Procedure for gene amplification of nucleotide sequences of viruses of the HIV-1 and/or HIV-2 and/or SIV type, performed starting from a biological sample, this procedure comprising mainly the following steps:

- a step involving the extraction of the nucleic acid to be detected belonging to the genome of the virus of the HIV-1, HIV-2 or SIV type possibly present in the above-mentioned biological sample and, where appropriate, a step involving treatment of the said nucleic acid with a reverse transcriptase if the former is in the form of RNA,
- a cycle comprising the following steps:
  . denaturation of the double-stranded nucleic acid to be detected, which leads to the formation of a single-stranded nucleic acid,
  . hybridization of each of the single-stranded nucleic acids

obtained during the preceding denaturation step with at least one primer according to one of the Claims 1 to 11, by placing the above-mentioned single-strands in contact with at least one of the above-mentioned primer couples,

. formation, starting from the primers, of the DNAs complementary to the single strands to which they are hybridized in the presence of a DNA polymerase and the four different nucleoside triphosphates (dNTPs), which leads to the formation of a greater number of double-stranded nucleic acids to be detected than at the preceding denaturation step, this cycle being repeated a specific number of times in order to obtain the said nucleic acid sequence to be detected possibly present in the biological sample in an amount sufficient to permit its detection,

- a step involving the detection of the possible presence of the nucleic acid belonging to the genome of the virus of the HIV-1 and/or HIV-2 and/or SIV type in the biological sample.

13. Procedure according to Claim 12, characterized in that the step involving the expression of the viral DNA comprises the following steps:

. suspension of the cell pellet in 0.5 ml of boiled water in a Potter homogenizer with a wide pestle,

. grinding of the cells by "forwards and backwards rotation",

. addition of Triton X100 to give a final concentration of 0.1%,

. heat denaturation for 15 to 25 minutes at 100°C,

. brief centrifugation in order to remove only the cell debris,

. precipitation of the DNA overnight at -20°C by the addition of 2.5 volumes of absolute ethanol and 10% of the final volume of 3 molar sodium acetate.

14. Procedure according to Claim 13, characterized in that the retro-transcription step of the viral RNA comprises the following steps:

- 10 µg of RNA, extracted and resuspended in water, are placed in the presence of the primer couple, each at a concentration of 0.8 µM, in a final volume of 40 µl; the mixture is denatured at 100°C for 10 minutes, then plunged into ice-cold water,

- 10 µl of the following mixture are added: 5 µl of the "10 X buffer" (containing, when it is diluted 1/10: Tris-HCl, pH = 8.9: 50 mM; $(NH_4)_2SO_4$: 15 mM; $MgCl_2$: 5 mM; ß-mercaptoethanol: 10 mM; gelatin: 0.25 mg/ml) + 1 unit of reverse transcriptase + 1 unit of Taq polymerase + 1 µl of a 25 mM mixture of each of the 4 dNTPs + water to give 10 µl; the synthesis of the cDNA results from the action of the reverse transcriptase at 42°C for 13 minutes, then the mixture is heated at 95°C for 3 minutes in order to destroy the reverse transcriptase.

15. Procedure according to one of the Claims 12 to 14, characterized in that the denaturation step is carried out in the presence of the primer couple(s) according to one of the Claims 1 to 11.

16. Procedure according to Claim 15, characterized in that it is performed under the following conditions:

- hybridization: the primers (1 µl of a 40 µmolar solution of each primer) are placed in the presence of the DNA-matrix (100 to 300 ng) for the first step of denaturation-reassociation; the tubes containing this mixture of DNA-matrix and primers are heated for 10 minutes at 100°C, then plunged into ice-cold water. The primers must be used at a final concentration of 0.8 µM each in the amplification step which follows.
- amplification: the 4 dNTPs, each being used at a concentration of 0.4 µmolar in the final solution (50 µl), and one unit of Taq polymerase per 50 µl of reaction mixture are added to the preceding mixture; this step is carried out in the amplification buffer designated by the name of "10 X buffer", the composition of which is given in Claim 14.

17. Use of the procedure according to any one of the Claims 12 to 16 for the in vitro diagnosis of the infection of an individual by a virus of the HIV-1 and/or HIV-2 type, or of an animal by at least one of the three viruses (HIV-1, HIV-2, SIV).

18. Use of the procedure according to any one of the Claims 12 to 16 for the amplification of nucleotide sequences of the genomes of the viruses of the HIV or SIV type, followed by the translation of these amplified sequences into proteins, starting from the nucleotide primers according to one of the Claims 1 to 11.

19. Immunogenic compositions containing one (or more) translation product of the nucleotide sequences according to one of the ~~Claims 1 to~~ 11, and/or one (or more) translation product of the nucleotide sequences amplified by the procedure according to one of the Claims 12 to 16.

20. The following oligonucleotide primer couples for the implementation of a method according to one of the Claims 12 to 16: MMy4Ba-MMy28a, MMy26-MMy5a, MMy8a-MMy89, MMy89a-MMy9a, MMy25-MMy27, MMy26-MMy27, MMy28-MMy29a, MMy29-MMy30a, MMy30-MMy31a, MMy31-MMy32a.

21. Kit for the implementation of a method according to one of the Claims 12 to 16 containing:
- at least one oligonucleotide primer couple according to any one of the Claims 1 to 11 or according to the Claim 20,
- suitable reagents for the implementation of a cycle of amplification operations, in particular DNA polymerase and the four different nucleotide triphosphates,
- 10 X buffer as described in Claim 14,
- one (or several) probe(s), which may be labelled, capable of hybridizing with the amplified nucleic acid sequence(s) to be detected.

22. Composition for the treatment of viral diseases, in particular AIDS, containing at least one anti-sense nucleotide sequence according to one of the Claims 1 to 11 in combination with a pharmaceutically acceptable vehicle.

23. Antibodies capable of giving rise to an immunological reaction with the translation products of the nucleotide sequences according to one of the Claims 1 to 11, and/or with one (or more) translation product(s) of the nucleotide sequences amplified by the method according to one of the Claims 12 to 16.

24. Method of in vitro diagnosis of the infection of an individual by a virus of the HIV-1 and/or HIV-2 type, or of an animal by at least one of the three viruses (HIV-1, HIV-2, SIV) comprising the placing of a biological sample (in particular serum) taken fr m a patient under study in contact with antibodies according to Claim 23, and the detection of the immunological complexes formed between the antigens of the viruses of the HIV or SIV type possibly present

in the biological sample and the said antibodies.

25. Kit for the implementation of a method according to Claim 24, containing antibodies according to Claim 23 and, where appropriate, suitable reagents for the detection of the immunological complex formed between the said antibodies and the antigens of the HIV and/or SIV viruses.

26. Buffer solution ("10 X buffer") for use in the hybridization step of the procedure according to Claim 12, or in the retrotranscription step of the viral RNA of the procedure according to Claim 14, characterized in that it is constituted, when diluted 1/10, of:

- Tris-HCl, pH 8.9: 50 mM;
- $(NH_4)_2SO_4$: 15 mM;
- $MgCl_2$: 5 mM;
- ß-mercaptoethanol: 10 mM;
- gelatin: 0.25 mg/ml.

Add α'

add β'

Add α3